SEQUENCE LISTING

(1) GENERAL INFORMATION:

    (i) APPLICANT: An, Gang
               O'Hara, S. Mark
               Ralph, David
               Veltri, Robert

    (ii) TITLE OF INVENTION: BIOMARKERS AND TARGETS FOR DIAGNOSIS,
           PROGNOSIS AND MANAGEMENT OF PROSTATE DISEASE

    (iii) NUMBER OF SEQUENCES: 87

    (iv) CORRESPONDENCE ADDRESS:
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        (E) COUNTRY: USA
        (F) ZIP: 77210

    (v) COMPUTER READABLE FORM:
        (A) MEDIUM TYPE: Floppy disk
        (B) COMPUTER: IBM PC compatible
        (C) OPERATING SYSTEM: PC-DOS/MS-DOS
        (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

    (vi) CURRENT APPLICATION DATA:
        (A) APPLICATION NUMBER: US Unknown
        (B) FILING DATE: Concurrently Herewith
        (C) CLASSIFICATION: Unknown

    (vii) PRIOR APPLICATION DATA:
        (A) APPLICATION NUMBER: US 08/692,787
        (B) FILING DATE: 31-JUL-1996

    (viii) ATTORNEY/AGENT INFORMATION:
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        (B) REGISTRATION NUMBER: P-42,023
        (C) REFERENCE/DOCKET NUMBER: UROC:018

    (ix) TELECOMMUNICATION INFORMATION:
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(2) INFORMATION FOR SEQ ID NO:1:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 391 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

126

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
GTCCAGTCGC TCAGAAATTT CCTTTGATGC TTTGAAGTTA TCTCTCTTGG ATCTGCTTCC     60

TCCTTATCGT CTCTACATCC CAAGAACAGA GAGTGAGTCT TCTTTATTTT CTTATCTCTG    120

TTTTTAGCAC AGTATTTGAT ATATAGTGTA GATACTATAA ATGCTTGCTA AACTTTGTCA    180

AATTCCACAT TTTTAAAATA AAAATGAGAA TGAGCTTGTA GTCAACATGG CGTTTGTAAG    240

TTTGGAGTCT ATATATGGTA GATATACATA TTTTTAAATC TAAGTGCAAC TTTTCTCTTG    300

ATTATCTTGA AATGCCTTAT CATCTCCACA TTTGCTGTAG GCAGTAGTTT AGTGGGTCCA    360

TTATATCTGC CACACTGATT GTCTTAAATA A                                    391
```

(2) INFORMATION FOR SEQ ID NO:2:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 614 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
CAGTAGTGGC CCCAAATGCC AGGCTGCACT GATATTTATT GGATATAAGA CAAAGGGGCA     60

GGGTAAGGAA TGTGAACCAT CTCCAATAAT AGGTAAGGTC ACATGGGTCA TGTGTCCACT    120

GGACAGGGGG CCCTTCCCTG CCTGGCAGCA GAGGCAGAGA GAGAGAGAAG AGAGAGAGAC    180

AGCTTATGCC ATTATTTCTG CATATCAGAC ATTTAGTACT TTCACTAATT TGCTCCTGCT    240

ATCTAAAAGG CAGAGCCAGG TATACAGGAT GGAACATGAA AGCGGACTAG GAGCGTGACC    300

ACTGAAGCAC AGCATCACAG GGAGACAGGC CTCTGGATAC TGGCCGGGGG GCCCTGACTG    360

ATGTCAAGGC CCTCCACAAG AGTGGAGGAG TTAGTCTTCC TCTAAACTCC CCCGGGGGAA    420

AGGGAGGCTC CTTTTCCCAG TCTGCTAAGT AGTGGGTGTT TTTCCTTGAC ACTGATGCTA    480

CTGCTAGACC ATGGTCCACT TTGCAACAGG CATCTTCCCA GACACTGGTG TTACTGCTAG    540

ACCAAGCCCT CTGGTGGCCC TGTCCGGGCA TAAGAGAAGG CTCACACTCT TGTCTTCTGG    600

CCACTTCGCA CTAT                                                      614
```

(2) INFORMATION FOR SEQ ID NO:3:

      (i) SEQUENCE CHARACTERISTICS:

127

(A) LENGTH: 757 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ACAACGACAC ATTCAGGAGT TAAATATTTA TCATCAAACA TTGGATTTTT CCTTAACGCT   60

AGAGATTGCT ACAAATCTTC TGAAGGGTCT CAATGGCTTC AGGCTAAGAA GAGATTTCTC   120

CCTGTTATAA GCAGCAAGAC AAATTAGCCA TTTCACTCTC AAACTTCACT AATGATCACA   180

TTCTTTCCAA AAGGAACTCT AGAAGACCAA ATGCCCCGAG TTAAGAACAT CAAAACTAAC   240

CATCTGAAGA AACTTCCCAA GTGTAAGACT CTGCCATTAA AACATTACCG AGAGGGGACT   300

CAAACAGTCT TTTCTTCCCT TTGTCGTGTT TCTTTGCTCC CAGACCCAAG GCACTTGGCG   360

GACAGTACTT GATACAATAA TTTAAAAAGC ACCACTCCCT TCCCACTTTG TAAATACCCA   420

GAACTCTAAT TGGACCACCC TGAAGCTTAG GACCTACCAG CCATACAAAT AGTAAACTCT   480

GTCCACGATT CACTCATCTG TGTATTTTCT ATAGATGTTT ACTAGGCGTT TGTTATATAA   540

AAATACCCCG GCCAGGCACG GTGGCTCACG CCTGTAATCC CAGCACTTTG GGAGGTGGGT   600

GGATCACCTG AGGTCGGGAG TTCGAGACCA GCCTGACCAG CATGGTGGAA CCCCCATCTC   660

TACTAAAAAC ACAAAAAATT AGCCGGGCGT GGTGGCACAT GCCTGTAATC CCAGCTACTC   720

AGGAGGCTGA GGCGGAGAAT TGCTTGAACC CGGAAGG   757

(2) INFORMATION FOR SEQ ID NO:4:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 673 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CAGGACACAG AGTAAGATAC CCACTGACTT CTTGTGGTCT ACTTCCTGGG TGTTGTTTCA   60

ATGGGCTTTG TTATAACAGG ACTAGTCTTC TGTAAATACA ACTTGGTAAA TAGGATGAAA   120

CATAACTTTG CGACAATTCA GTAGAAATAG GCATACAAAC CTGGGCCTGA TGACACTCAC   180

CTCCCCTTGG CTATAAACAT TACCCTACCT GTTAAGTCAG TAATCCTTTG GGAGAGCGCT   240

TACTGAGTAT CTATGATATG CAAAGACCAA AGACCGAGGG GGATCCCTGG TGTAGAGCAA   300

128

A: 148244(36DW01!.DOC)

GCACACACCT GGTTATTAGC TACCTGCCAC CCTGCTGGGC ATGCAACATA CATTGTCTCA   360

AATTCTAACC ACCCTGCAAG GCAAGCTTCC TTGTTCTTTT AAAGAAGAAA AGTAGACCAG   420

CAAGATTGAT TTGCTCAAGA TTACACAGCC TGGAATCTTG TCATGGGCAT GTCTGACTCT   480

GATAGCAATA CCCTCAAAGA AACTGTCAGA GAAGACTCAA TAAGAAGAAA GTTGAGATAC   540

AGAAACCAAC AGGAGAAGGT AATTCAGAAA TTCAAACAGA GTGGGTGTGA TGGGAAGAAT   600

TCATTAATAA GAAGGTACCT CTGTAGAAAA ATCTTACCAG ACAGTCTGGA AGTGAAGGAA   660

ACAGCCAATA GTC   673

(2) INFORMATION FOR SEQ ID NO:5:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 358 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GTCACTGCAC ATTAAGATGG AGCCCGAAGA GCCACACTCC GAGGGGGCAT CGCAGGAGGA   60

TGGGGCTCAA GGTGCCTGGG GCTGGGCACC CCTAAGTCAC GGCTCTAAGG AGAAAGCTCT   120

CTTCCTGCCC GGCGGAGCCC TCCCCTCCCC CCGGATCCCC GTGCTTTCCC GAGAGGGGAG   180

GACCAGAGAC CGGCAGATGG CTGCAGCGCT CCTCACTGCC TGGTCCCAGA TGCCAGTGAC   240

TTTCGAGGAT GTGGCCTTGT ACCTCTCCCG GGAGGAGTGG GGACGGCTGG ACCACACGCA   300

GCAGAACTTC TACAGGGAAT GTCCTGCAGA AGAAAAATGG GCTGTCACTG GGCTTTCC   358

(2) INFORMATION FOR SEQ ID NO:6:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 23 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CACAGATGTA GCTTCCTCAC TGG   23

(2) INFORMATION FOR SEQ ID NO:7:

        (i) SEQUENCE CHARACTERISTICS:

129

A: 148244(36DW01!.DOC)

```
            (A)  LENGTH: 610 base pairs
            (B)  TYPE: nucleic acid
            (C)  STRANDEDNESS: single
            (D)  TOPOLOGY: linear

      (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:7:

CTGGAGTACA ATGTCAGTGT TTACACTGTC AAGGATGACA AGGAAAGTGT CCCTATCTCT      60

GATACCATCA TCCCAGCTGT TCCTCCTCCC ACTGACCTGC GATTCACCAA CATTGGTCCA     120

GACACCATGC GTGTCACCTG GGCTCCACCC CCATCCATTG ATTTAACCAA CTTCCTGGTG     180

CGTTACTCAC CTGTGAAAAA TGAGGAAGAT GTTGCAGAGT TGTCAATTTC TCCTTCAGAC     240

AATGCAGTGG TCTTAACAAA TCTCCTGCCT GGTACAGAAT ATGTAGTGAG TGTCTCCAGT     300

GTCTACGAAC AACATGAGAG CACACCTCTT AGAGGAAGAC AGAAACAGG TCTTGATTCC      360

CCAACTGGCA TTGACTTTTC TGATATTACT GCCAACTCTT TTACTGTGCA CTGGATTGCT     420

CCTCGAGCCA CCATCACTGG CTACAGGATC CGCCATCATC CCGAGCACTT CAGTGGGAGA     480

CCTCGAGAAG ATCGGGTGCC CCACTCTCGG AATTCCATCA CCCTCACCAA CCTCACTCCA     540

GGCACAGAGT ATGTGGTCAG CATCGTTGCT CTTAATGGCA GAGAGGAAAG TCCCTTATTG     600

ATTGGCCAAC                                                           610


(2)  INFORMATION FOR SEQ ID NO:8:

      (i)  SEQUENCE CHARACTERISTICS:
            (A)  LENGTH: 1649 base pairs
            (B)  TYPE: nucleic acid
            (C)  STRANDEDNESS: single
            (D)  TOPOLOGY: linear

      (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:8:

CGGCAGCCAG CCTATTCTTT GGCCGGGTCG GTGCGAGTGG TCGGCTGGGC AGAGTGCACG      60

CTGCTTGGCG CCGCAGGTGA TCCCGCCGTC CACTCCCGGG AGCAGTGATG TTGGGCAACT     120

CTGCGCCGGG GCCTGCGACC CGCGAGGCGG GCTCGGCGCT GCTAGCATTG CAGCAGACGG     180

CGCTCCAAGA GGACCAGGAG AATATCAACC CGGAAAAGGC AGCGCCCGTC CAACAACCGC     240

GGACCCGGGC CGCGCTGGCG GTACTGAAGT CCGGGAACCC GCGGGGTCTA GCGCAGCAGC     300

AGAGGCCGAA GACGAGACGG GTTGCACCCC TTAAGGATCT TCCTGTAAAT GATGAGCATG     360

TCACCGTTCC TCCTTGGAAA GCAAACAGTA AACAGCCTGC GTTCACCATT CATGTGGATG     420
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130

AAGCAGAAAA AGAAGCTCAG AAGAAGCCAG CTGAATCTCA AAAAATAGAG CGTGAAGATG   480

CCCTGGCTTT TAATTCAGCC ATTAGTTTAC CTGGACCCAG AAAACCATTG GTCCCTCTTG   540

ATTATCCAAT GGATGGTAGT TTTGAGTCAC CACATACTAT GGACATGTCA ATTGTATTAG   600

AAGATGAAAA GCCAGTGAGT GTTAATGAAG TACCAGACTA CCATGAGGAT ATTCACACAT   660

ACCTTAGGGA AATGGAGGTT AAATGTAAAC CTAAAGTGGG TTACATGAAG AAACAGCCAG   720

ACATCACTAA CAGTATGAGA GCTATCCTCG TGGACTGGTT AGTTGAAGTA GGAGAAGAAT   780

ATAAACTACA GAATGAGACC CTGCATTTGG CTGTGAACTA CATTGATAGG TTCCTGTCTT   840

CCATGTCAGT GCTGAGAGGA AAACTTCAGC TTGTGGGCAC TGCTGCTATG CTGTTAGCCT   900

CAAAGTTTGA AGAAATATAC CCCCCAGAAG TAGCAGAGTT TGTGTACATT ACAGATGATA   960

CCTACACCAA GAAACAAGTT CTGAGAATGG AGCATCTAGT TTTGAAAGTC CTTACTTTTG   1020

ACTTAGCTGC TCCAACAGTA AATCAGTTTC TTACCCAATA CTTTCTGCAT CAGCAGCCTG   1080

CAAACTGCAA AGTTGAAAGT TTAGCAATGT TTTTGGGAGA ATTAAGTTTG ATAGATGCTG   1140

ACCCATACCT CAAGTATTTG CCATCAGTTA TTGCTGGAGC TGCCTTTCAT TTAGCACTCT   1200

ACACAGTCAC GGGACAAAGC TGGCCTGAAT CATTAATACG AAAGACTGGA TATACCCTGG   1260

AAAGTCTTAA GCCTTGTCTC ATGGACCTTC ACCAGACCTA CCTCAAAGCA CCACAGCATG   1320

CACAACAGTC AATAAGAGAA AAGTACAAAA ATTCAAAGTA TCATGGTGTT TCTCTCCTCA   1380

ACCCACCAGA GACACTAAAT CTGTAACAAT GAAAGACTGC CTTTGTTTTC TAAGATGTAA   1440

ATCACTCAAA GTATATGGTG TACAGTTTTT AACTTAGGTT TTTAATTTTA CAATCATTTC   1500

TGAATACAGA AGTTGTGGCC AAGTACAAAT TATGGTATCT ATTACTTTTT AAATGGTTTT   1560

AATTTGTATA TCTTTTGTAT ATGTATCTGT CTTAGATATT TGGCTAATTT TAAGTGGTTT   1620

TGTTAAAGTA TTAATGATGC CAGCTGCCG   1649

(2) INFORMATION FOR SEQ ID NO:9:

        (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 175 base pairs
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: single
              (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ACCCACTCGT GAGTCCAACG GTCTTTTCTG CAGAAAGGAG GACTTTCCTT TCAGGGGTCT   60

131

TTCTGGGGCT CTTACTATAA AAGGGGACCA ACTCTCCCTT TGTCATATCT TGTTTCTGAT   120

GACAAAAAAT AACACATTGT TAAAATTGTA AAATTAAAAC ATGAAATATA AATTA   175

(2) INFORMATION FOR SEQ ID NO:10:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 166 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GTTTCGCTCC ACATTCATCC TTTCTTACTG GGCACTGATG TTGAGAGCAT CAGGCAGGGT   60

ATAATGTTAT GTTGCAGTAA CAAACACCCT CAATATCTCA GTGGCTTAAA ATGACAACGA   120

TCTTTTTTTT GTTTGTTTGT TTATGCTCTA TATCACCCAG GGATCA   166

(2) INFORMATION FOR SEQ ID NO:11:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 107 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TGCTCTGCCC CACATCTGAA CAAGCTAATA AGAAAGCCCG ATGTTCTTTC CTTTGGTGCC   60

ATTGGGAAAT TCAAACCATG CACAACTCTG CCTGTATGAA GGGCGCA   107

(2) INFORMATION FOR SEQ ID NO:12:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 183 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CAACCTTAGC CCCTCTCCTC TTCTTCACGA TGCCATTCTG CCATTTCTGT TTTGTGGTAG   60

ACAGGTTGGC CCAGGCACTC TAAGGCCCAG GCTGGCACAG GTTGGCCCAG GCACTTCAAG   120

CCTAAGTCCA TTTACAGTTT CTATTCCATC TCTTCCTAAA GAAGAGGAGA GGGGCTAAGG   180

132

(2) INFORMATION FOR SEQ ID NO:13:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 92 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AAACAAACGT CTTTGGGTAA AATTCTATTT CTTTTAATGT TTTAAAATAT TTGTAGTCAC   60

TAATTGTAAG TCATATTCCT CTTTGTCCAG CT   92

(2) INFORMATION FOR SEQ ID NO:14:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 182 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GATGTAATTA AAGCTGTAGA TGAGGGCTAT CGACTGCCAC CCCCCATGGA CTGCCCAGCT   60

GCCTTGTATC AGCTGATGCT GGACTGCTGG CAGAAAGACA GGAACAACAG ACCCAAGTTT   120

GAGCAGATTG TTAGTATTCT GGACAAGCTT ATCCGGAATC CCGGCAGCCT GAAGGATCAT   180

CA   182

(2) INFORMATION FOR SEQ ID NO:15:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 174 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GCCAAATGGG TAGCATTGTT GCTCGGCCTT CTAGTCTGCC AGTAGGAAAG TCCAACCATT   60

AGGTCGGGGA AGAAGGGTCT GGATTTGGTT GACAATGGTT GGATGGGGGA TAGAAGCAGA   120

GAGAGAGAGG GAGGGCAGCT CAAGGGTATC TTGCCCCACT CTGTTTATGC TGAT   174

(2) INFORMATION FOR SEQ ID NO:16:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 132 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CACCTAACAA TATATCAATT TTTTAAAAAT GGAATTTCTT ATGCCCTCTT TATTTATGGA   60

CATGTATGTC CATAATGGGA GACGTTTTCT TTGGACTGAT GCTTGAATCA GTGGGTGCTT   120

GGCATTGCTG AT   132

(2) INFORMATION FOR SEQ ID NO:17:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 135 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CAGACACACA CATGCACACC ATTCTAGAAT GCTTCCTTAA AAGAAGGAGG GTTGCCCTAG   60

TCTCAAAATC TTAAAAGCCA TATGTGCATT GATTTCTGCA CAGGTAGGCA ATTTGTGATT   120

TTATTTTTCC TTATG   135

(2) INFORMATION FOR SEQ ID NO:18:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 24 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CTTCATGGCA GGACTCGGTT TGGG   24

(2) INFORMATION FOR SEQ ID NO:19:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 471 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

134

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

```
GCCCCAAATG CCAGGCTGCA CTGATCTCAT GTCTGTGTCA CTGGAACCAA CAGGCCTGCC        60

TCAACCACTG TCCACCTGCA CATCTGAGAG GCTGGCAGGT CACCAGGGCT AGCCGTGCAC       120

GTCAGTTCCT GGGAAGAAAG TAGAATGTGA ATCATCTTCT CTCAAACGCC TATCAAAAGC       180

CCAGCTGAGA TCAATAATTT GGTGGGAGAA CAGACCTGTA CCAATTGGCT CGGTGTTTGG       240

TGGGGTATTG TAAATTTGGA TCCTAAATCA AAGGGTATCC CTAGAAGGAC CCACATGGAA       300

TGGCCTCCTC CTAAACATCC CTCCATGTTG GTACTTCCTG ACTCTTTTCC AGCAATCTCA       360

AAGCACAAGA AGCAGTGGTG GGAACCCAGG CCTGGCATCT TGTTGGAGCC CATGGTTGGG       420

GGGTAGGAGC AACTTTACAG GCCATCAATT ATGCCCCTAT ACGCACCTCC C               471
```


(2) INFORMATION FOR SEQ ID NO:20:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 209 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

```
GCCCTTTATA AATACGATTA GTATGGAGAA TTGATACATT AACAGTTAGC TTTATAAATT        60

GACAGATTTC TAAATTAACC TATGGTCCAC AAATCAAGTT CTATCACTAT TTCCTGCCAC       120

CAAAATCAGT GATGAAGCCT CTCCCACACT AAATGAAGAG TGGCGAGGGA CAGAATTCCA       180

CTTGTCTTCC TTTTGCTGCA CTAACTACA                                        209
```


(2) INFORMATION FOR SEQ ID NO:21:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 407 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

```
CAAGCAGCAT AGCCTCTCTG AAACTCAATT TCCTCACATT TATAAATGAG CTTTTATATT        60

ATTTACAAAC CTACCTCATA GAGCAGGTTG CAGGCTACAT GAGAAGGTGC AAGTTCAATG       120

CCAAGCAGGG TCCTAGTATT TAATAAAAGC TCAATAAATA TTCATTTTCT TCTTTCCTTC       180
```

135

TCTTACTTGA AGTATAACAT TTGATAATGA ATTTTCTCAT TGCAACAATA ACACCCCTTC   240

CACTGAGGGA TTTGTATCCC TGCTTAAGAA GCTATTAGTA TTCTACAGCA GGACTCACCC   300

CACACAATCT TGGCAGGAAT ACATCCCTCT ACCTCTCTGG TCAATAACCT GCCTGGCCTG   360

TGACCCCAGG CTTCCTGGAG AAGCACCAAG TCCTCCCAGT TTCCCCC   407

(2) INFORMATION FOR SEQ ID NO:22:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 267 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CATTGGTGCA GCAGGTTTAG ATGGCTATGT GCTAGAGTAT TGCTTTGAAG GAAGTAAGTA   60

CAACCAGTAG ATAAAATGAA TACTGTCATC AATAGGTGAG ATATGTCCCT CCCCTTTCTG   120

TTGTCTCTCT TTCTTGAGAA CGCATCACCT TCCTACGAAA ATAAGATCAA GCCAAACGTC   180

ATCCTTCTGA GATGTATATA AACTAAGCCC TTTTTTAGTA CTTGGTGCTT ATAAATTGAT   240

ATCTCAAAAG TATCTTGGCT AGGCTGC   267

(2) INFORMATION FOR SEQ ID NO:23:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 333 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CATAGTCCAG GAGCAGAGTT AGCCAGAATT GCCTCCTGCT GCCCCAGCTT AGAGAGCTCC   60

CATCTCAATC ATTGAGCCTG AAGGCTTCAA GCCCAAAATG CAACAAGACC CCCAGCCTAC   120

ATTTCTCAGC TCCCCTGGAG CCAGTGATCC TGTAACGCTG CTGGAGGTCA GTCTGAGCTA   180

CCAAGACTGT CCCTAGACAA AGGTGGGAGT CCCCCACACT GCCAAGACCA AATCCCTCAC   240

TCAACCTGCT GAGGTGTTGG ATGGGGAAAC AAGAGGCAAA ACTGAGGCAC CTGATGCATT   300

CAGCCCTGCT TGTGCAGAAG TGCATTGACT GCC   333

136

(2) INFORMATION FOR SEQ ID NO:24:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 21 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: single
       (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CCTGTGGCGT AAGGCATCCC A   21

(2) INFORMATION FOR SEQ ID NO:25:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 25 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: single
       (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GCAAGCACTC CTTTGTAAAA TGTCC   25

(2) INFORMATION FOR SEQ ID NO:26:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 29 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: single
       (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

TGCGTTCACC ATTCATGTGG ATGAAGCAG   29

(2) INFORMATION FOR SEQ ID NO:27:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 28 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: single
       (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CTCCTACTTC AACTAACCAG TCCACGAG   28

(2) INFORMATION FOR SEQ ID NO:28:

A: 148244(36DW011.DOC)

```
      (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 25 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: single
           (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GATGCTTTGA AGTTATCTCT CTTGG                                          25


 (2) INFORMATION FOR SEQ ID NO:29:

      (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 25 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: single
           (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

ATCAGTGTGG CAGATATAAT GGACC                                          25


 (2) INFORMATION FOR SEQ ID NO:30:

      (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 25 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: single
           (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GCCCCAAATG CCAGGCTGCA CTGAT                                          25


 (2) INFORMATION FOR SEQ ID NO:31:

      (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 25 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: single
           (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GCCAGAAGAC AAGAGTGTGA GCCTT                                          25


 (2) INFORMATION FOR SEQ ID NO:32:

      (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 25 base pairs
```

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                (B)  TYPE: nucleic acid
                (C)  STRANDEDNESS: single
                (D)  TOPOLOGY: linear

        (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:32:

GCTTCAGGGT GGTCCAATTA GAGTT                                          25


(2)  INFORMATION FOR SEQ ID NO:33:

        (i)  SEQUENCE CHARACTERISTICS:
                (A)  LENGTH: 25 base pairs
                (B)  TYPE: nucleic acid
                (C)  STRANDEDNESS: single
                (D)  TOPOLOGY: linear

        (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:33:

TCCAACAACG ACACATTCAG GAGTT                                          25


(2)  INFORMATION FOR SEQ ID NO:34:

        (i)  SEQUENCE CHARACTERISTICS:
                (A)  LENGTH: 25 base pairs
                (B)  TYPE: nucleic acid
                (C)  STRANDEDNESS: single
                (D)  TOPOLOGY: linear

        (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:34:

GGACACAGAG TAAGATACCC ACTGA                                          25


(2)  INFORMATION FOR SEQ ID NO:35:

        (i)  SEQUENCE CHARACTERISTICS:
                (A)  LENGTH: 25 base pairs
                (B)  TYPE: nucleic acid
                (C)  STRANDEDNESS: single
                (D)  TOPOLOGY: linear

        (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:35:

CCTCGGTCTT TGGTCTTTGC ATATC                                          25


(2)  INFORMATION FOR SEQ ID NO:36:

        (i)  SEQUENCE CHARACTERISTICS:
                (A)  LENGTH: 25 base pairs
                (B)  TYPE: nucleic acid
                (C)  STRANDEDNESS: single
```

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(D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

ACAAGGAAAG TGTCCCTATC TCTGA   25

    (2) INFORMATION FOR SEQ ID NO:37:

        (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 25 base pairs
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: single
              (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

CTCGAGGTCT CCCACTGAAG TGCTC   25

    (2) INFORMATION FOR SEQ ID NO:38:

        (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 25 base pairs
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: single
              (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

CACTGCACAT TAAGATGGAG CCCGA   25

    (2) INFORMATION FOR SEQ ID NO:39:

        (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 25 base pairs
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: single
              (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

CCTGTAGAAG TTCTGCTGCG TGTGG   25

    (2) INFORMATION FOR SEQ ID NO:40:

        (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 25 base pairs
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: single
              (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CGAGCTGCCT GACGGCCAGG TCATC   25

(2) INFORMATION FOR SEQ ID NO:41:

        (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 25 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: single
             (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GAAGCATTTG CGGTGGACGA TGGAG   25

(2) INFORMATION FOR SEQ ID NO:42:

        (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 22 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: single
             (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

TAGAAGACCA AATGCCCCGA GT   22

(2) INFORMATION FOR SEQ ID NO:43:

        (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 22 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: single
             (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

TGTATTTCTG TGGGATCGGT GG   22

(2) INFORMATION FOR SEQ ID NO:44:

        (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 25 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: single
             (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

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(2) INFORMATION FOR SEQ ID NO:45:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 369 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

CCATAAGAGA AATGATTGGT AGGTTTGCAT GAAATTTTAA AATTTCCTGT GGCGTAAGGC   60

ATCCCATAAC GAAGCCAAAA GGTGAGTGAT AGACTGGGAG AAATAACTGC CAGACGTTGC   120

CAGACAAAGA TTTCATATTT CTAATATGCT AGAGTACCTT TAATTTGATA AGAAAAAGAT   180

AAGCAATCCT GTAATAAAAT GGACATTTTA CAAAGGAGTG CTTGCAAATG GCCAGTGAAT   240

TTATGCAAAT ATGTTCAGGG AAATAGGAAT GAAAACGAGA TTCCACTTTT TCATCATCCA   300

TTTGATTGGC AAGAAATTTT TAAAAGAGTA ATACCTAGTG AATCACTCAT GTAGGAAAAT   360

GGGTTGGTG   369

(2) INFORMATION FOR SEQ ID NO:46:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 301 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ix) FEATURE:
        (A) NAME/KEY: modified_base
        (B) LOCATION: 212
        (D) OTHER INFORMATION: /note= "N = A, C, G, or T"

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

GCCCTTGAAG AGTGTAACCA AGAAGCATCT CTCAATCAAT GAACCTGAGA CAGCCTGTTC   60

ACTTCTGACC ATCATTCTTG TCCTTTAGAT CTCAGTTTCA AATTCATTTC TTCTAGACAT   120

TCATCTCTTC CCATGTTTAA TCTGGAACCA TCTACCCTTC CACCAGACCA ATTATCCTGG   180

CAAATTAATG TAATAGACCA GTATTAATTA TNTGGTTGTA TGTCTTAACA ACATTCTAGG   240

TGCTGTGCCA AAAACAAATG AATAGCAACA CAAGGTCTTC TTGGTTACAC TCTTCAAGGG   300

C   301

(2) INFORMATION FOR SEQ ID NO:47:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 3061 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ix) FEATURE:
        (A) NAME/KEY: CDS
        (B) LOCATION: 15..1172

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

```
CGGCTCTCCT CAAC ATG AGA GCT GCA CCC CTC CTC CTG GCC AGG GCA GCA        50
                Met Arg Ala Ala Pro Leu Leu Leu Ala Arg Ala Ala
                  1             5              10

AGC CTT AGC CTT GGC TTC TTG TTT CTG CTT TTT TTC TGG CTA GAC CGA        98
Ser Leu Ser Leu Gly Phe Leu Phe Leu Leu Phe Phe Trp Leu Asp Arg
            15              20              25

AGT GTA CTA GCC AAG GAG TTG AAG TTT GTG ACT TTG GTG TTT CGG CAT       146
Ser Val Leu Ala Lys Glu Leu Lys Phe Val Thr Leu Val Phe Arg His
        30              35              40

GGA GAC CGA AGT CCC ATT GAC ACC TTT CCC ACT GAC CCC ATA AAG GAA       194
Gly Asp Arg Ser Pro Ile Asp Thr Phe Pro Thr Asp Pro Ile Lys Glu
    45              50              55              60

TCC TCA TGG CCA CAA GGA TTT GGC CAA CTC ACC CAG CTG GGC ATG GAG       242
Ser Ser Trp Pro Gln Gly Phe Gly Gln Leu Thr Gln Leu Gly Met Glu
                65              70              75

CAG CAT TAT GAA CTT GGA GAG TAT ATA AGA AAG AGA TAT AGA AAA TTC       290
Gln His Tyr Glu Leu Gly Glu Tyr Ile Arg Lys Arg Tyr Arg Lys Phe
            80              85              90

TTG AAT GAG TCC TAT AAA CAT GAA CAG GTT TAT ATT CGA AGC ACA GAC       338
Leu Asn Glu Ser Tyr Lys His Glu Gln Val Tyr Ile Arg Ser Thr Asp
        95              100             105

GTT GAC CGG ACT TTG ATG AGT GCT ATG ACA AAC CTG GCA GCC CTG TTT       386
Val Asp Arg Thr Leu Met Ser Ala Met Thr Asn Leu Ala Ala Leu Phe
    110             115             120

CCC CCA GAA GGT GTC AGC ATC TGG AAT CCT ATC CTA CTC TGG CAG CCC       434
Pro Pro Glu Gly Val Ser Ile Trp Asn Pro Ile Leu Leu Trp Gln Pro
125             130             135             140

ATC CCG GTG CAC ACA GTT CCT CTT TCT GAA GAT CAG TTG CTA TAC CTG       482
Ile Pro Val His Thr Val Pro Leu Ser Glu Asp Gln Leu Leu Tyr Leu
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CCT TTC AGG AAC TGC CCT CGT TTT CAA GAA CTT GAG AGT GAG ACT TTG        530
Pro Phe Arg Asn Cys Pro Arg Phe Gln Glu Leu Glu Ser Glu Thr Leu
            160                 165                 170

AAA TCA GAG GAA TTC CAG AAG AGG CTG CAC CCT TAT AAG GAT TTT ATA        578
Lys Ser Glu Glu Phe Gln Lys Arg Leu His Pro Tyr Lys Asp Phe Ile
            175                 180                 185

GCT ACC TTG GGA AAA CTT TCA GGA TTA CAT GGC CAG GAC CTT TTT GGA        626
Ala Thr Leu Gly Lys Leu Ser Gly Leu His Gly Gln Asp Leu Phe Gly
            190                 195                 200

ATT TGG AGT AAA GTC TAC GAC CCT TTA TAT TGT GAG AGT GTT CAC AAT        674
Ile Trp Ser Lys Val Tyr Asp Pro Leu Tyr Cys Glu Ser Val His Asn
205                 210                 215                 220

TTC ACT TTA CCC TCC TGG GCC ACT GAG GAC ACC ATG ACT AAG TTG AGA        722
Phe Thr Leu Pro Ser Trp Ala Thr Glu Asp Thr Met Thr Lys Leu Arg
                225                 230                 235

GAA TTG TCA GAA TTG TCC CTC CTG TCC CTC TAT GGA ATT CAC AAG CAG        770
Glu Leu Ser Glu Leu Ser Leu Leu Ser Leu Tyr Gly Ile His Lys Gln
            240                 245                 250

AAA GAG AAA TCT AGG CTC CAA GGG GGT GTC CTG GTC AAT GAA ATC CTC        818
Lys Glu Lys Ser Arg Leu Gln Gly Gly Val Leu Val Asn Glu Ile Leu
            255                 260                 265

AAT CAC ATG AAG AGA GCA ACT CAG ATA CCA AGC TAC AAA AAA CTT ATC        866
Asn His Met Lys Arg Ala Thr Gln Ile Pro Ser Tyr Lys Lys Leu Ile
            270                 275                 280

ATG TAT TCT GCG CAT GAC ACT ACT GTG AGT GGC CTA CAG ATG GCG CTA        914
Met Tyr Ser Ala His Asp Thr Thr Val Ser Gly Leu Gln Met Ala Leu
285                 290                 295                 300

GAT GTT TAC AAC GGA CTC CTT CCT CCC TAT GCT TCT TGC CAC TTG ACG        962
Asp Val Tyr Asn Gly Leu Leu Pro Pro Tyr Ala Ser Cys His Leu Thr
            305                 310                 315

GAA TTG TAC TTT GAG AAG GGG GAG TAC TTT GTG GAG ATG TAC TAT CGG        1010
Glu Leu Tyr Phe Glu Lys Gly Glu Tyr Phe Val Glu Met Tyr Tyr Arg
            320                 325                 330

AAT GAG ACG CAG CAC GAG CCG TAT CCC CTC ATG CTA CCT GGC TGC AGC        1058
Asn Glu Thr Gln His Glu Pro Tyr Pro Leu Met Leu Pro Gly Cys Ser
            335                 340                 345

CCT AGC TGT CCT CTG GAG AGG TTT GCT GAG CTG GTT GGC CCT GTG ATC        1106
Pro Ser Cys Pro Leu Glu Arg Phe Ala Glu Leu Val Gly Pro Val Ile
            350                 355                 360
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CCT CAA GAC TGG TCC ACG GAG TGT ATG ACC ACA AAC AGC CAT CAA GGT          1154
Pro Gln Asp Trp Ser Thr Glu Cys Met Thr Thr Asn Ser His Gln Gly
365             370             375             380

ACT GAG GAC AGT ACA GAT TAGTGTGCAC AGAGATCTCT GTAGAAAGAG                  1202
Thr Glu Asp Ser Thr Asp
            385


TAGCTGCCCT TTCTCAGGGC AGATGATGCT TTGAGAACAT ACTTTGGCCA TTACCCCCCA        1262

GCTTTGAGGA AAATGGGCTT TGGATGATTA TTTTATGTTT TAGGGACCCC CAACCTCAGG        1322

CAATTCCTAC CTCTTCACCT GACCCTGCCC CCACTTGCCA TAAAACTTAG CTAAGTTTTG        1382

TTTTGTTTTT CAGCGTTAAT GTAAAGGGGC AGCAGTGCCA AAATATAATC AGAGATAAAG        1442

CTTAGGTCAA AGTTCATAGA GTTCCCATGA ACTATATGAC TGGCCACACA GGATCTTTTG        1502

TATTTAAGGA TTCTGAGATT TTGCTTGAGC AGGATTAGAT AAGTCTGTTC TTTAAATTTC        1562

TGAAATGGAA CAGATTTCAA AAAAAATTCC CACAATCTAG GGTGGGAACA AGGAAGGAAA        1622

GATGTGAATA GGCTGATGGG GAAAAAACCA ATTTACCCAT CAGTTCCAGC CTTCTCTCAA        1682

GGAGAGGCAA AGAAAGGAGA TACAGTGGAG ACATCTGGAA AGTTTTCTCC ACTGGAAAAC        1742

TGCTACTATC TGTTTTTATA TTTCTGTTAA AATATATGAG GCTACAGAAC TAAAAATTAA        1802

AACCTCTTTG TGTCCCTTGG TCCTGGAACA TTTATGTTCC TTTTAAAGAA ACAAAAATCA        1862

AACTTTACAG AAAGATTTGA TGTATGTAAT ACATATAGCA GCTCTTGAAG TATATATATC        1922

ATAGCAAATA AGTCATCTGA TGAGAACAAG CTATTTGGGC ACAACACATC AGGAAAGAGA        1982

GCACCACGTG ATGGAGTTTC TCCAGAAGCT CCAGTGATAA GAGATGTTGA CTCTAAAGTT        2042

GATTTAAGGC CAGGCATGGT GGTTTACGCC TATAATCCCA GCATTTTGGG ACTCCGAGGT        2102

GGGCAGATCA CTTGAGCTCA GGAGCTCAAG ATCAGCCTGG GCAACATGGT GAAACCTTGT        2162

CTCTACATAA AATACAAAAA CTTAGATGGG CATGGTGCTG TGTGCCTATA GTCCACTACT        2222

TGTGGGGCTA AGGCAGGAGG ATCACTTGAG CCCCGGAGGT CGAGGCTACA GTGACCCAAG        2282

AGTGCACTAC TGTACTCCAG CCAGGGCAAG AGAGCGAGAC CCTGTCTCAA TAAATAAATA        2342

AATAAATAAA TAAATAAATA AATAAAAACA AAGTTGATTA AGAAAGGAAG TATAGGCCAG        2402

GCACAGTGGC TCACACCTGT AATCCTTGCA TTTTGGAAGG CTGAGGCAGG AGGATCACTT        2462

TAGGCCTGGT GTGTTCAAGA CCAGCCTGGT CAACATAGTG AGACACTGTC TCTACCAAAA        2522

AAAGGAAGGA AGGGACACAT ATCAAACTGA AACAAAATTA GAAATGTAAT TATGTTATGT        2582
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TCTAAGTGCC TCCAAGTTCA AAACTTATTG GAATGTTGAG AGTGTGGTTA CGAAATACGT   2642

TAGGAGGACA AAAGGAATGT GTAAGTCTTT AATGCCGATA TCTTCAGAAA ACCTAAGCAA   2702

ACTTACAGGT CCTGCTGAAA CTGCCCACTC TGCAAGAAGA AATCATGATA TAGCTTTCCA   2762

TGTGGCAGAT CTACATGTCT AGAGAACACT GTGCTCTATT ACCATTATGG ATAAAGATGA   2822

GATGGTTTCT AGAGATGGTT TCTACTGGCT GCCAGAATCT AGAGCAAAGC CATCCCCCCT   2882

CCTGGTTGGT CACAGAATGA CTGACAAAGA CATCGATTGA TATGCTTCTT TGTGTTATTT   2942

CCCTCCCAAG TAAATGTTTG TCCTTGGGTC CATTTTCTAT GCTTGTAACT GTCTTCTAGC   3002

AGTGAGCCAA ATGTAAAATA GTGAATAAAG TCATTATTAG GAAGTTCAAA AAAAAAAA   3061

(2) INFORMATION FOR SEQ ID NO:48:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 386 amino acids
            (B) TYPE: amino acid
            (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: protein

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Met Arg Ala Ala Pro Leu Leu Leu Ala Arg Ala Ala Ser Leu Ser Leu
1   5   10   15

Gly Phe Leu Phe Leu Leu Phe Phe Trp Leu Asp Arg Ser Val Leu Ala
                20   25   30

Lys Glu Leu Lys Phe Val Thr Leu Val Phe Arg His Gly Asp Arg Ser
        35   40   45

Pro Ile Asp Thr Phe Pro Thr Asp Pro Ile Lys Glu Ser Ser Trp Pro
    50   55   60

Gln Gly Phe Gly Gln Leu Thr Gln Leu Gly Met Glu Gln His Tyr Glu
65   70   75   80

Leu Gly Glu Tyr Ile Arg Lys Arg Tyr Arg Lys Phe Leu Asn Glu Ser
                85   90   95

Tyr Lys His Glu Gln Val Tyr Ile Arg Ser Thr Asp Val Asp Arg Thr
            100   105   110

Leu Met Ser Ala Met Thr Asn Leu Ala Ala Leu Phe Pro Pro Glu Gly
        115   120   125

Val Ser Ile Trp Asn Pro Ile Leu Leu Trp Gln Pro Ile Pro Val His
    130   135   140

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Thr Val Pro Leu Ser Glu Asp Gln Leu Leu Tyr Leu Pro Phe Arg Asn
145                 150             155                 160

Cys Pro Arg Phe Gln Glu Leu Glu Ser Glu Thr Leu Lys Ser Glu Glu
                165                 170                 175

Phe Gln Lys Arg Leu His Pro Tyr Lys Asp Phe Ile Ala Thr Leu Gly
            180                 185                 190

Lys Leu Ser Gly Leu His Gly Gln Asp Leu Phe Gly Ile Trp Ser Lys
            195                 200                 205

Val Tyr Asp Pro Leu Tyr Cys Glu Ser Val His Asn Phe Thr Leu Pro
    210                 215                 220

Ser Trp Ala Thr Glu Asp Thr Met Thr Lys Leu Arg Glu Leu Ser Glu
225                 230                 235                 240

Leu Ser Leu Leu Ser Leu Tyr Gly Ile His Lys Gln Lys Glu Lys Ser
            245                 250                 255

Arg Leu Gln Gly Gly Val Leu Val Asn Glu Ile Leu Asn His Met Lys
            260                 265                 270

Arg Ala Thr Gln Ile Pro Ser Tyr Lys Lys Leu Ile Met Tyr Ser Ala
            275                 280                 285

His Asp Thr Thr Val Ser Gly Leu Gln Met Ala Leu Asp Val Tyr Asn
    290                 295                 300

Gly Leu Leu Pro Pro Tyr Ala Ser Cys His Leu Thr Glu Leu Tyr Phe
305                 310                 315                 320

Glu Lys Gly Glu Tyr Phe Val Glu Met Tyr Tyr Arg Asn Glu Thr Gln
            325                 330                 335

His Glu Pro Tyr Pro Leu Met Leu Pro Gly Cys Ser Pro Ser Cys Pro
            340                 345                 350

Leu Glu Arg Phe Ala Glu Leu Val Gly Pro Val Ile Pro Gln Asp Trp
            355                 360                 365

Ser Thr Glu Cys Met Thr Thr Asn Ser His Gln Gly Thr Glu Asp Ser
    370                 375                 380

Thr Asp
385
```

(2) INFORMATION FOR SEQ ID NO:49:

   (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 22 base pairs

```
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

TCGCTCCACA TTCATCCTTT CT                                                      22


(2) INFORMATION FOR SEQ ID NO:50:

     (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 25 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

TGATCCCTGG GTGATATAGA GCATA                                                   25


(2) INFORMATION FOR SEQ ID NO:51:

     (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 25 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GCCCCACATC TGAACAAGCT AATAA                                                   25


(2) INFORMATION FOR SEQ ID NO:52:

     (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 25 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

TGCGCCCTTC ATACAGGCAG AGTTG                                                   25


(2) INFORMATION FOR SEQ ID NO:53:

     (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 25 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
```

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(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

CACGATGCCA TTCTGCCATT TCTGT   25

(2) INFORMATION FOR SEQ ID NO:54:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 25 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

GGAAGAGATG GAATAGAAAC TGTAA   25

(2) INFORMATION FOR SEQ ID NO:55:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 23 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

CTTAACTCGG GCATTTGGTC TTC   23

(2) INFORMATION FOR SEQ ID NO:56:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 21 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

    Arg Lys Lys Glu Lys Val Lys Arg Ser Gln Lys Ala Thr Glu Phe Ile
    1   5   10   15

    Asp Tyr Ser Ile Glu
                20

(2) INFORMATION FOR SEQ ID NO:57:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 27 base pairs

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(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

CACTGGAACC AACAGGCCTG CCTCAAC   27

(2) INFORMATION FOR SEQ ID NO:58:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 30 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

CCGAGCCAAT TGGTACAGGT CTGTTCTCCC   30

(2) INFORMATION FOR SEQ ID NO:59:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 28 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

CCTCAAGACT GGTCCACGGA GTGTATGA   28

(2) INFORMATION FOR SEQ ID NO:60:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 30 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

GGGTAATGGC CAAAGTATGT TCTCAAAGCA   30

(2) INFORMATION FOR SEQ ID NO:61:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 21 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single

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(D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

AAACAAACGT CTTTGGGTAA A   21

  (2) INFORMATION FOR SEQ ID NO:62:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 20 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

CTGGACAAAG AGGAATATGA   20

  (2) INFORMATION FOR SEQ ID NO:63:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 28 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

GCCCTTTATA AATACGATTA GTATGGAG   28

  (2) INFORMATION FOR SEQ ID NO:64:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 25 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

TGTAGTTAGT GCAGCAAAAG GAAGA   25

  (2) INFORMATION FOR SEQ ID NO:65:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 26 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

GATGTAATTA AAGCTGTAGA TGAGGG   26

(2) INFORMATION FOR SEQ ID NO:66:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 28 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

GAATACTAAC AATCTGCTCA AACTTGGG   28

(2) INFORMATION FOR SEQ ID NO:67:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 26 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

GCCAAATGGG TAGCATTGTT GCTCGG   26

(2) INFORMATION FOR SEQ ID NO:68:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 25 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

CAGAGTGGGG CAAGATACCC TTGAG   25

(2) INFORMATION FOR SEQ ID NO:69:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 21 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

AATGGAATTT CTTATGCCCT C   21

(2) INFORMATION FOR SEQ ID NO:70:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 23 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

CAATGCCAAG CACCCACTGA TTC   23

(2) INFORMATION FOR SEQ ID NO:71:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 24 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

ACACAGACAC ACACATGCAC ACCA   24

(2) INFORMATION FOR SEQ ID NO:72:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 20 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

CCTACCTGTG CAGAAATCAA   20

(2) INFORMATION FOR SEQ ID NO:73:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 24 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

AGCAGCATAG CCTCTCTGAA ACTC   24

153

(2) INFORMATION FOR SEQ ID NO:74:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 27 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

CCTTCTCATG TAGCCTGCAA CCTGCTC   27

(2) INFORMATION FOR SEQ ID NO:75:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 24 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

CATTGGTGCA GCAGGTTTAG ATGG   24

(2) INFORMATION FOR SEQ ID NO:76:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 25 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

GAGATATCAA TTTATAAGCA CCAAG   25

(2) INFORMATION FOR SEQ ID NO:77:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 23 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

ATCTCAATCA TTGAGCCTGA AGG   23

(2) INFORMATION FOR SEQ ID NO:78:

154

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        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 24 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

CAGCAGGTTG AGTGAGGGAT TTGG                                                24


    (2) INFORMATION FOR SEQ ID NO:79:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 22 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

CGCCTCAGGC TGGGGCAGCA TT                                                  22


    (2) INFORMATION FOR SEQ ID NO:80:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 25 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

ACAGTGGAAG AGTCTCATTC GAGAT                                               25


    (2) INFORMATION FOR SEQ ID NO:81:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 25 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

CGAGCTGCCT GACGGCCAGG TCATC                                               25


    (2) INFORMATION FOR SEQ ID NO:82:

        (i) SEQUENCE CHARACTERISTICS:
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155

(A) LENGTH: 25 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: single
                (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

GAAGCATTTG CGGTGGACGA TGGAG   25

(2) INFORMATION FOR SEQ ID NO:83:

        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 2087 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: single
                (D) TOPOLOGY: linear

        (ix) FEATURE:
                (A) NAME/KEY: CDS
                (B) LOCATION: 99..503

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

GACCTTAAAT ATATCGAGGT GGCTAATTGA TGTATAATAA TTTACAAAAT TATTCTTCTA   60

TTGCTACAGA GCTACAATTC AATTTACAGT AGGCCACC ATG AGG GCC TTC TTA   113
                                            Met Arg Ala Phe Leu
                                            1   5

AGG AAC CAG AAA TAT GAG GAT ATG CAC AAT ATT ATT CAC ATT TTA CAG   161
Arg Asn Gln Lys Tyr Glu Asp Met His Asn Ile Ile His Ile Leu Gln
            10   15   20

ATC AGA AAA TTG AGG CAC AGA TTA AGT AAC TTC CCA AGG CTA CCA GGC   209
Ile Arg Lys Leu Arg His Arg Leu Ser Asn Phe Pro Arg Leu Pro Gly
            25   30   35

ATT CTA GCT CCA GAA ACT GTG CTC TTA CCA TTC TGC TAC AAG GTA TTT   257
Ile Leu Ala Pro Glu Thr Val Leu Leu Pro Phe Cys Tyr Lys Val Phe
            40   45   50

CGA AAA AAA GAA AAA GTA AAA AGA AGT CAA AAG GCA ACA GAG TTC ATT   305
Arg Lys Lys Glu Lys Val Lys Arg Ser Gln Lys Ala Thr Glu Phe Ile
    55   60   65

GAT TAT TCC ATA GAA CAG TCA CAC CAT GCA ATT CTC ACA CCC TTG CAG   353
Asp Tyr Ser Ile Glu Gln Ser His His Ala Ile Leu Thr Pro Leu Gln
70   75   80   85

ACA CAC TTG ACC ATG AAA GGT TCC TCA ATG AAA TGT TCC TCA TTA TCT   401
Thr His Leu Thr Met Lys Gly Ser Ser Met Lys Cys Ser Ser Leu Ser
                90   95   100

                                    156

A: 148244(36DW011.DOC)

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TCA GAA GCC ATA TTA TTC ACA TTG ACT TTG CAG TTA ACT CAG ACC CTA      449
Ser Glu Ala Ile Leu Phe Thr Leu Thr Leu Gln Leu Thr Gln Thr Leu
            105                 110                 115

GGT CTG GAA TGC TGT CTT CTC TAC TTA TCC AAA ACT ATA CAT CCA CAG      497
Gly Leu Glu Cys Cys Leu Leu Tyr Leu Ser Lys Thr Ile His Pro Gln
            120                 125                 130

ATC ATA TAAACTCTCA GCCCTGCTGC AAAGCCTTTC CAGAAAAATA AAAATGGTTG       553
Ile Ile
    135

AAAAGGCAAT TCTGCTACCA ATGACTGTTT AAGCCCAGCC AAGTAACTGA ACCATTCCAA     613

CTTCAATTTA CTTATGAAAA GAATTTGATG ATGTAGGAGG TTATTTCAAT TCTAAAATAC     673

AAACCCATGT TGATCTTTCT CAATCTTGAA CTCATAGATT ATTATCTATT ATCTCAATTT     733

AGTTTGTTAT TTATCCTAGT GGGCCATTAA AAACTACCAC ATGTGTTTCT GTCTCTCCAT     793

TAGTCAATAA CTAAACTAAC GAGCAATTAG TAAGCCATGT GCCAGATGCT CCGCTAGGCA     853

CCAGAGGGAT AAAAACAATA CTTATAGTAT ACCACTAATT TTCGCTTAGT AACTAGTGAA    · 913

ATGTTCAAGT CATGCCTGAG TCAAGAGTTG AGGAGACATT ACAATGTGTA ATGGAAACCA     973

AGGAAAGTGA AACTTTGGAT AAGTGGGGAC TAGTGTATTT ATATATTTAA TTGATTTCTG    `1033

ACTCTATCAT TGGCCTCCAA ACACAGATTG TGTTTTTCTT TGGTTTTGTT TTCTTCACTA     1093

TGGGATCTTC TGTGCCCAGC ACAGTGCCTG ACACATAGAA AACAATCAAT ATTTGCTGAA     1153

TAAATGATTA AAAAATCAGA GAACTTTCCC ATTCTGTTTG GATCTATAGA ACATCCAGAG     1213

TAAGTGATGA GGGCCTCTGC ATTTATATGC GCTTAAATTA AGATTATGTG AGAAAAGTTT     1273

AAAGACACTT AGTAGAGTGA TTTTGAAATA TAGTAAACAC TTGGAAATGG TGGTGCTTTA     1333

AAAAGATATT AATAGATAAT ATGAAAATCT CCATCTCAAA AATAATGCAT AAACTATTTA     1393

AAGGAAAATC ACATCTCCAG GCTTTCAATG TTTGTTCATT ACTTTTTCAT ATATTTTTAC     1453

CATCTGCTGA AGGCAGTCAT ATCAAAGGGT AAAGAAAGAT GGGAGGAAAA CTCAGTAAGA     1513

ATTATATTAG TCTGTTTGCA AAGTAGAAAA AGATTCTCAT CACTCAACCT TATGAGCAGG     1573

AAGAGGGAAG GCTGTTTGAG AACCATTTAC TTAGCAGAAC CACATATTTT AGACACTTCC    . 1633

CTGCATTAAC TGCACAAACA ATATGTTTGC AAACTTGTTG ATCAACCTCC AACAACGACA     1693

CATTCAGGAG TTAAATATTT TTCATCAAAC ATTGGATTTT TCCTTAACGC TAGAGATTGC     1753

TACAAATCTT CTGAAGGGTC TCAATGGCTT CAGGCTAAGA AGAGATTTCT CCCTGTTATA     1813
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AGCAGCAAGA CAAATTAGCC ATTTCACTCT CAAACTTCAC TAATGATCAC ATTCTTTCCA   1873

AAAGGAACTC TAGAAGACCA AATGCCCCGA GTTAAGAACA TCAAAACTAA CCATCTGAAG   1933

AAACTTCCCA AGTGTAAGAC TCTGCCTGCA CGACAACACA TAAAAAAAGA GAGAAGAATC   1993

AAATAGACAC AATAAAAAAT GATAAAGGGG ATATCACCAC CGATCCCACA GAAATACAAA   2053

CTACCATCAG AGAATACTAC AAACACCTCT ACGC   2087

(2) INFORMATION FOR SEQ ID NO:84:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 135 amino acids
            (B) TYPE: amino acid
            (D) TOPOLOGY: linear

       (ii) MOLECULE TYPE: protein

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

Met Arg Ala Phe Leu Arg Asn Gln Lys Tyr Glu Asp Met His Asn Ile
 1   5   10   15

Ile His Ile Leu Gln Ile Arg Lys Leu Arg His Arg Leu Ser Asn Phe
                20   25   30

Pro Arg Leu Pro Gly Ile Leu Ala Pro Glu Thr Val Leu Leu Pro Phe
            35   40   45

Cys Tyr Lys Val Phe Arg Lys Lys Glu Lys Val Lys Arg Ser Gln Lys
        50   55   60

Ala Thr Glu Phe Ile Asp Tyr Ser Ile Glu Gln Ser His His Ala Ile
65   70   75   80

Leu Thr Pro Leu Gln Thr His Leu Thr Met Lys Gly Ser Ser Met Lys
                85   90   95

Cys Ser Ser Leu Ser Ser Glu Ala Ile Leu Phe Thr Leu Thr Leu Gln
            100   105   110

Leu Thr Gln Thr Leu Gly Leu Glu Cys Cys Leu Leu Tyr Leu Ser Lys
            115   120   125

Thr Ile His Pro Gln Ile Ile
    130   135

(2) INFORMATION FOR SEQ ID NO:85:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 2505 base pairs

A: 148244(36DW011.DOC)

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        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ix) FEATURE:
        (A) NAME/KEY: CDS
        (B) LOCATION: 99..503

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

GACCTTAAAT ATATCGAGGT GGCTAATTGA TGTATAATAA TTTACAAAAT TATTCTTCTA        60

TTGCTACAGA GCTACAATTC AATTTACAGT AGGCCACC ATG AGG GCC TTC TTA           113
                                          Met Arg Ala Phe Leu
                                           1                 5

AGG AAC CAG AAA TAT GAG GAT ATG CAC AAT ATT ATT CAC ATT TTA CAG        161
Arg Asn Gln Lys Tyr Glu Asp Met His Asn Ile Ile His Ile Leu Gln
                10                  15                  20

ATC AGA AAA TTG AGG CAC AGA TTA AGT AAC TTC CCA AGG CTA CCA GGC        209
Ile Arg Lys Leu Arg His Arg Leu Ser Asn Phe Pro Arg Leu Pro Gly
                25                  30                  35

ATT CTA GCT CCA GAA ACT GTG CTC TTA CCA TTC TGC TAC AAG GTA TTT        257
Ile Leu Ala Pro Glu Thr Val Leu Leu Pro Phe Cys Tyr Lys Val Phe
                40                  45                  50

CGA AAA AAA GAA AAA GTA AAA AGA AGT CAA AAG GCA ACA GAG TTC ATT        305
Arg Lys Lys Glu Lys Val Lys Arg Ser Gln Lys Ala Thr Glu Phe Ile
            55                  60                  65

GAT TAT TCC ATA GAA CAG TCA CAC CAT GCA ATT CTC ACA CCC TTG CAG        353
Asp Tyr Ser Ile Glu Gln Ser His His Ala Ile Leu Thr Pro Leu Gln
70                  75                  80                  85

ACA CAC TTG ACC ATG AAA GGT TCC TCA ATG AAA TGT TCC TCA TTA TCT        401
Thr His Leu Thr Met Lys Gly Ser Ser Met Lys Cys Ser Ser Leu Ser
                    90                  95                  100

TCA GAA GCC ATA TTA TTC ACA TTG ACT TTG CAG TTA ACT CAG ACC CTA        449
Ser Glu Ala Ile Leu Phe Thr Leu Thr Leu Gln Leu Thr Gln Thr Leu
                105                 110                 115

GGT CTG GAA TGC TGT CTT CTC TAC TTA TCC AAA ACT ATA CAT CCA CAG        497
Gly Leu Glu Cys Cys Leu Leu Tyr Leu Ser Lys Thr Ile His Pro Gln
                120                 125                 130

ATC ATA TAAACTCTCA GCCCTGCTGC AAAGCCTTTC CAGAAAAATA AAAATGGTTG          553
Ile Ile
        135

AAAAGGCAAT TCTGCTACCA ATGACTGTTT AAGCCCAGCC AAGTAACTGA ACCATTCCAA       613

                                      159
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CTTCAATTTA CTTATGAAAA GAATTTGATG ATGTAGGAGG TTATTTCAAT TCTAAAATAC        673

AAACCCATGT TGATCTTTCT CAATCTTGAA CTCATAGATT ATTATCTATT ATCTCAATTT        733

AGTTTGTTAT TTATCCTAGT GGGCCATTAA AAACTACCAC ATGTGTTTCT GTCTCTCCAT        793

TAGTCAATAA CTAAACTAAC GAGCAATTAG TAAGCCATGT GCCAGATGCT CCGCTAGGCA        853

CCAGAGGGAT AAAAACAATA CTTATAGTAT ACCACTAATT TTCGCTTAGT AACTAGTGAA        913

ATGTTCAAGT CATGCCTGAG TCAAGAGTTG AGGAGACATT ACAATGTGTA ATGGAAACCA        973

AGGAAAGTGA AACTTTGGAT AAGTGGGGAC TAGTGTATTT ATATATTTAA TTGATTTCTG       1033

ACTCTATCAT TGGCCTCCAA ACACAGATTG TGTTTTTCTT TGGTTTTGTT TTCTTCACTA       1093

TGGGATCTTC TGTGCCCAGC ACAGTGCCTG ACACATAGAA AACAATCAAT ATTTGCTGAA       1153

TAAATGATTA AAAAATCAGA GAACTTTCCC ATTCTGTTTG GATCTATAGA ACATCCAGAG       1213

TAAGTGATGA GGGCCTCTGC ATTTATATGC GCTTAAATTA AGATTATGTG AGAAAAGTTT       1273

AAAGACACTT AGTAGAGTGA TTTTGAAATA TAGTAAACAC TTGGAAATGG TGGTGCTTTA       1333

AAAAGATATT AATAGATAAT ATGAAAATCT CCATCTCAAA AATAATGCAT AAACTATTTA       1393

AAGGAAAATC ACATCTCCAG GCTTTCAATG TTTGTTCATT ACTTTTTCAT ATATTTTTAC       1453

CATCTGCTGA AGGCAGTCAT ATCAAAGGGT AAAGAAAGAT GGGAGGAAAA CTCAGTAAGA       1513

ATTATATTAG TCTGTTTGCA AAGTAGAAAA AGATTCTCAT CACTCAACCT TATGAGCAGG       1573

AAGAGGGAAG GCTGTTTGAG AACCATTTAC TTAGCAGAAC CACATATTTT AGACACTTCC       1633

CTGCATTAAC TGCACAAACA ATATGTTTGC AAACTTGTTG ATCAACCTCC AACAACGACA       1693

CATTCAGGAG TTAAATATTT TTCATCAAAC ATTGGATTTT TCCTTAACGC TAGAGATTGC       1753

TACAAATCTT CTGAAGGGTC TCAATGGCTT CAGGCTAAGA AGAGATTTCT CCCTGTTATA       1813

AGCAGCAAGA CAAATTAGCC ATTTCACTCT CAAACTTCAC TAATGATCAC ATTCTTTCCA       1873

AAAGGAACTC TAGAAGACCA AATGCCCCGA GTTAAGAACA TCAAAACTAA CCATCTGAAG       1933

AAACTTCCCA AGTGTAAGAC TCTGCCATTA AAACATTACC GAGAGGGGAC TCAAACAGTC       1993

TTTCTTCCTT TGTCGTGTTT CTTGCTCCCA GACCAAGGCA CTGACGACAG TACTGATACA       2053

TAATTTAAAA GCACACTCCC TTCCACTTTG GTAATACCAG AACTCTAATT GGACCACCCT       2113

GAAGCTTAGG ACTACCAGCC ATACAAATAG TAAACTCTGT CCACGATTCA CTCATCTGTG       2173

TATTTTCTAT AGATGTTTAC TAGGCGTTTG TTATATAAAA ATACCCCGGC CAGGCACGGT       2233
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GGCTCACGCC TGTAATCCCA GCACTTTGGG AGGTGGGTGG ATCACCTGAG GTCGGGAGTT   2293

CGAGACCAGC CTGACCAGCA TGGTGGAACC CCCATCTCTA CTAAAAACAC AAAAAATTAG   2353

CCGGGCGTGG TGGCACATGC CTGTAATCCC AGCTACTCAG GAGGCTGAGG CGGAGAATTG   2413

CTTGAACCCG GAAGGTGGAG GTTGTTGCGG TGAGCTGAGA TTGCACTATT GCACTCCAGC   2473

CTGGGCAACA GGAGTAAAAC TCCCCCCCAC CC   2505

(2) INFORMATION FOR SEQ ID NO:86:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 135 amino acids
            (B) TYPE: amino acid
            (D) TOPOLOGY: linear

       (ii) MOLECULE TYPE: protein

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Met Arg Ala Phe Leu Arg Asn Gln Lys Tyr Glu Asp Met His Asn Ile
 1   5   10   15

Ile His Ile Leu Gln Ile Arg Lys Leu Arg His Arg Leu Ser Asn Phe
            20   25   30

Pro Arg Leu Pro Gly Ile Leu Ala Pro Glu Thr Val Leu Leu Pro Phe
        35   40   45

Cys Tyr Lys Val Phe Arg Lys Lys Glu Lys Val Lys Arg Ser Gln Lys
    50   55   60

Ala Thr Glu Phe Ile Asp Tyr Ser Ile Glu Gln Ser His His Ala Ile
65   70   75   80

Leu Thr Pro Leu Gln Thr His Leu Thr Met Lys Gly Ser Ser Met Lys
                85   90   95

Cys Ser Ser Leu Ser Ser Glu Ala Ile Leu Phe Thr Leu Thr Leu Gln
            100   105   110

Leu Thr Gln Thr Leu Gly Leu Glu Cys Cys Leu Leu Tyr Leu Ser Lys
        115   120   125

Thr Ile His Pro Gln Ile Ile
    130   135

(2) INFORMATION FOR SEQ ID NO:87:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 22 base pairs

161

A: 148244(36DW011.DOC)

(B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

CCCACCTCCC AAAGTGCTGG GA   22